

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 27, 2001, 16:39:12 ; Search time 26.6 seconds
(without alignments)
910.658 million cell updates/sec

Title: US-09-483-543A-8
Perfect score: 1693
Sequence: 1 KRGGAGNFDSEERSWYGR.....QGNFDEDFSCGXGLEVLQF 318
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5 C_{rk}

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1612	95.2	304	2 I58394	c-Crk - mouse
2	1588	93.8	304	2 A45022	CRK-II - human
3	1379.5	81.5	305	1 A49011	c-Crk - chicken
4	1078	63.7	239	2 A46243	epidermal growth f
5	1052	62.1	204	2 B45022	CRK-I - human
6	917.5	54.2	303	2 S41754	CRKL protein - hum
7	911.5	53.8	303	2 S58352	SH2/SH3 adaptor pr
8	834.5	49.3	259	2 A44988	transforming prote
9	818.5	48.3	232	1 TVFV10	transforming prote
10	236	13.9	211	2 A46444	SH2-SH3 adaptor pr
11	224	13.2	217	2 S26050	growth factor rece
12	224	13.2	217	2 A54688	modular adaptor cr
13	224	13.2	217	2 A43321	growth factor rece
14	218	12.9	217	2 JT0664	growth factor rece
15	202	11.9	228	2 S25730	SH2-SH3 protein se
16	184	10.9	1291	2 S00566	1-phosphatidylinos
17	182	10.8	1097	2 T31504	hypothetical prote
18	178	10.5	1290	2 A36466	1-phosphatidylinos
19	177	10.5	1290	2 A31317	1-phosphatidylinos
20	172.5	10.2	839	1 TVHUVV	transforming prote
21	170	10.0	816	2 T17257	hypothetical prote
22	167	9.9	844	1 TVMSVV	transforming prote
23	165	9.7	1270	2 T09194	adaptor protein in
24	164	9.7	1196	2 T14108	SH3-containing pro
25	161	9.5	1094	2 T13053	dynamain associated
26	158.5	9.4	330	2 JE0376	Grb-2 related adap
27	154.5	9.1	878	2 I51940	gene VAV2 protein
28	152.5	9.0	1011	2 T13055	dynamain associated
29	151.5	8.9	334	2 T33836	hypothetical prote

RESULT 1	151	8.9	1168	1 MWAXIC
I58394	150	8.9	960	1 A39651
c-Crk - mouse	149	8.8	639	2 T13151
C:Species: Mus sp. (mouse)	148.5	8.8	1113	1 A47106
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999	148	8.7	290	2 T42526
C:Accession: I58394	148	8.7	443	2 T27877
R:Ogawa, S.; Toyoshima, H.; Kozutsumi, H.; Hagiwara, K.; Sakai, R.; Tanaka, T.; Hiran	147	8.7	1044	2 S01966
Oncogene 9, 1669-1678, 1994	146.5	8.7	1038	2 JT0663
A:Title: The C-terminal SH3 domain of the mouse c-Crk protein negatively regulates ty	146	8.6	946	2 I38100
A:Reference number: I58394; MUID:94239744	144.5	8.5	1047	2 A40121
A:Accession: I58394	143.5	8.5	870	2 B40121
A:Status: preliminary; translated from GB/EMBL/DBJ	142	8.4	450	2 A41973
A:Molecule type: mRNA	141	8.3	665	2 JC7191
A:Residues: 1-304 <RES>	139.5	8.2	1236	1 A53970
A:Cross-references: GB:S72408; MID:g632866; PIDN:AAB30755.1; PID:g632867	139	8.2	359	2 S27788
C:Genetics:	139	8.2	557	2 A00629
C:Gene: c-crk				
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology				
F:13-118/Domain: SH2 homology <SH2>				
F:139-187/Domain: SH3 homology <SH3>				

Query Match	95.2%;	Score	1612;	DB 2;	Length	304;			
Best Local Similarity	100.0%;	Pred. No.	3.1e-113;						
Matches	303;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	5	AGNFDSEERSWYGRLSRQEAVALQQRHGCVFLVRDSSSTSPGDYVLSVSENSRVSHYI	64						
Db	2	AGNFDSEERSWYGRLSRQEAVALQQRHGCVFLVRDSSSTSPGDYVLSVSENSRVSHYI	61						
QY	65	INSSGPRPPVPPSPAOPPGVSPSLRIGDQFDSLPALEFYKTHYLDTTTTLIEPVARS	124						
Db	62	INSSGPRPPVPPSPAOPPGVSPSLRIGDQFDSLPALEFYKTHYLDTTTTLIEPVARS	121						
QY	125	ROGSGVILLRQEEAEYVRALDFNGNDEEDLPFKGDIILIRDKPBEQWNAEDSGKRG	184						
Db	122	ROGSGVILLRQEEAEYVRALDFNGNDEEDLPFKGDIILIRDKPBEQWNAEDSGKRG	181						
QY	185	IPVPVVKYRPASASVSALIGNQEGSHPPQLGGPEPGYAPQPSVNTPLNLQNGPIYAR	244						
Db	182	IPVPVVKYRPASASVSALIGNQEGSHPPQLGGPEPGYAPQPSVNTPLNLQNGPIYAR	241						
QY	245	VIQKRPVNPAYDKTALALEVGVLVKTKINVSGWEGECNGKRGHPFFTHVRLLLDQGNPDE	304						
Db	242	VIQKRPVNPAYDKTALALEVGVLVKTKINVSGWEGECNGKRGHPFFTHVRLLLDQGNPDE	301						
QY	305	DFS	307						
Db	302	DFS	304						
RESULT	2								

A45022
CRK-II - human
C:Species: Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 20-Jun-2000
C:Accession: A45022
R:Matsumura, M.; Tanaka, S.; Nagata, S.; Kojima, A.; Kurata, T.; Shibuya, M.
Mol. Cell. Biol. 12, 3482-3489, 1992
A:Title: Two species of human CRK cDNA encode proteins with distinct biological activities
A:Reference number: A45022; MUID:92334347
A:Accession: A45022
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-304 <MAT>
A:Cross-references: GB:D10656; NID:g219554; PIDN:BAA01505.1; PID:g219555
A:Experimental source: Placenta
A>Note: sequence extracted from NCBI backbone (NCBIN:108769, NCBIPI:108770)
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
F:13-118/Domain: SH2 homology #status atypical <SH2>
F:139-187/Domain: SH3 homology <SH3>

Query Match 93.8%; Score 1588; DB 2; Length 304;
Best Local Similarity 98.7%; Pred. No. 1.9e-111;
Matches 299; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 AGNFDSEERSWYGRSLRQEAVALLOGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 64
DB 2 AGNFDSEERSWYGRSLRQEAVALLOGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 61

QY 65 INSSGPRPPVPPSPAOPPGVSPSLRIGDQEFDSLPALEFYKIHLYDTTTLIEPVARS 124
DB 62 INSSGPRPPVPPSPAOPPGVSPSLRIGDQEFDSLPALEFYKIHLYDTTTLIEPVARS 121

QY 125 RQSGVILRQEAAYRVALDFNGNDEEDLPFKGDILIRDKPEEQWNAEDSEGRGM 184
DB 122 RQSGVILRQEAAYRVALDFNGNDEEDLPFKGDILIRDKPEEQWNAEDSEGRGM 181

QY 185 IPVPYVEKYRPAASVSALIGNGQSGHPQLGGPEPGYPAQPSVNTPLPLNONGPIYA 244
DB 182 IPVPYVEKYRPAASVSALIGNGQSGHPQLGGPEPGYPAQPSVNTPLPLNONGPIYA 241

QY 245 VTQKRVPNAYDKTALAELVGVKVTIKVNSQWEGECNGKRGHPFTHVRLDQONPD 304
DB 242 VTQKRVPNAYDKTALAELVGVKVTIKVNSQWEGECNGKRGHPFTHVRLDQONPD 301

QY 305 DFS 307
DB 302 DFS 304

RESULT 3
A49011
c-Crk - chicken
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49011
R:Reichman, C.T.; Mayer, B.J.; Keshav, S.; Hanafusa, H.
Cell Growth Differ. 3, 451-460, 1992
A:Title: The product of the cellular crk gene consists primarily of SH2 and SH3 regions.
A:Reference number: A49011; MUID:93041379
A:Accession: A49011
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-305 <REI>
A:Cross-references: GB:L08168; GB:M32398; NID:g212527; PIDN:AAA49001.1; PID:g212528
A:Experimental source: embryo, brain
A>Note: sequence extracted from NCBI backbone (NCBIN:117106, NCBIPI:117107)
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
F:13-119/Domain: SH2 homology <SH2>
F:140-188/Domain: SH3 homology <SH3>

Query Match 81.5%; Score 1379.5; DB 1; Length 305;

Best Local Similarity 84.5%; Pred. No. 7.2e-96;
Matches 257; Conservative 19; Mismatches 27; Indels 1; Gaps 1;

QY 5 AGNFDSEERSWYGRSLRQEAVALLOGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 64
DB 2 AGNFDSEERSWYGRSLRQEAVALLOGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 61

QY 65 INSSGPRPPVPPSPAOPPGVSPSLRIGDQEFDSLPALEFYKIHLYDTTTLIEPVARS 123
DB 62 INSSGPRPPVPPSPAOPPGVSPSLRIGDQEFDSLPALEFYKIHLYDTTTLIEPVARS 121

QY 124 RQSGVILRQEAAYRVALDFNGNDEEDLPFKGDILIRDKPEEQWNAEDSEGRGM 183
DB 122 RQSGVILRQEAAYRVALDFNGNDEEDLPFKGDILIRDKPEEQWNAEDSEGRGM 181

QY 184 MIPVYVEKYRPAASVSALIGNGQSGHPQLGGPEPGYPAQPSVNTPLPLNONGPIYA 243
DB 182 MIPVYVEKYRPAASVSALIGNGQSGHPQLGGPEPGYPAQPSVNTPLPLNONGPIYA 241

QY 244 VTQKRVPNAYDKTALAELVGVKVTIKVNSQWEGECNGKRGHPFTHVRLDQONPD 303
DB 242 VTQKRVPNAYDKTALAELVGVKVTIKVNSQWEGECNGKRGHPFTHVRLDQONPD 301

QY 304 DFS 307
DB 302 DFS 305

RESULT 4
A46243
epidermal growth factor-receptor-binding protein GRB-3 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 12-Feb-1999
C:Accession: A46243
R:Hargolis, B.; Silvennoinen, O.; Comoglio, F.; Roonprapant, C.; Skolnik, E.; Ullrich
Proc. Natl. Acad. Sci. U.S.A. 89, 8894-8898, 1992
A:Title: High-efficiency expression/cloning of epidermal growth factor-receptor-bind
A:Reference number: A46243; MUID:93028373
A:Accession: A46243
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-239 <WAR>
A>Note: sequence extracted from NCBI backbone (NCBIPI:115326)
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
C:Keywords: growth factor receptor
F:44-149/Domain: SH2 homology <SH2>
F:170-218/Domain: SH3 homology <SH3>

Query Match 63.7%; Score 1078; DB 2; Length 239;
Best Local Similarity 99.5%; Pred. No. 1.8e-73;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGNFDSEERSWYGRSLRQEAVALLOGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 64
DB 33 AGNFDSEERSWYGRSLRQEAVALLOGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 92

QY 65 INSSGPRPPVPPSPAOPPGVSPSLRIGDQEFDSLPALEFYKIHLYDTTTLIEPVARS 124
DB 93 INSSGPRPPVPPSPAOPPGVSPSLRIGDQEFDSLPALEFYKIHLYDTTTLIEPVARS 152

QY 125 RQSGVILRQEAAYRVALDFNGNDEEDLPFKGDILIRDKPEEQWNAEDSEGRGM 184
DB 153 RQSGVILRQEAAYRVALDFNGNDEEDLPFKGDILIRDKPEEQWNAEDSEGRGM 212

QY 185 IPVPYVEKYRPAASVSALIGNGQSG 211
DB 213 IPVPYVEKYRPAASVSALIGNGQSG 239

RESULT 5
B45022
CRK-I - human

C:Species: Homo sapiens (man)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 12-Feb-1999
C:Accession: B45022
R:Matsumura, M.; Tanaka, S.; Nagata, S.; Kojima, A.; Kurata, T.; Shibuya, M.
Mol. Cell. Biol. 12, 3482-3489, 1992
A:Title: Two species of human CRK cDNA encode proteins with distinct biological activities
A:Reference number: A45022; MUID:92334347
A:Accession: B45022
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-204 <MAT>
A:Experimental source: embryonic lung cells
A>Note: sequence extracted from NCBI backbone (NCBIN:108771, NCBI:108772)
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
F:13-118/Domain: SH2 homology <SH2>
F:139-187/Domain: SH3 homology <SH3>

Query Match 62.1%; Score 1052; DB 2; Length 204;
Best Local Similarity 99.0%; Pred. No. 1.3e-71;
Matches 200; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGNFDSEERSWYGLSRQEAVALLOGRGVFLVRDSTSPGDYVLSVSENSRVSHYI 64
DB 2 AGNFDSEERSWYGLSRQEAVALLOGRGVFLVRDSTSPGDYVLSVSENSRVSHYI 61

QY 65 INSSGPRPPVPPSPAPQPPGVPSRLRGDQEFDSLPALEFYKIHLYDITTTLIEPVARS 124
DB 62 INSSGPRPPVPPSPAPQPPGVPSRLRGDQEFDSLPALEFYKIHLYDITTTLIEPVARS 121

QY 125 RQSGVILRQEAAYVRALEDFNGNDEEDLPFKKGDILIRDKPQEWNAEDSEGKRG 184
DB 122 RQSGVILRQEAAYVRALEDFNGNDEEDLPFKKGDILIRDKPQEWNAEDSEGKRG 181

QY 185 IPVPVVEKYRPAASVSALIGG 206
DB 182 IPVPVVEKYRPAASVSALIGG 203

RESULT 6
S41754
CRKL protein - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S41754
R:ten Hoeve, J.; Morris, C.; Heisterkamp, N.; Groffen, J.
Oncogene 8, 2469-2474, 1993
A:Title: Isolation and chromosomal localization of CRKL, a human crk-like gene.
A:Reference number: S41754; MUID:93368949
A:Accession: S41754
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-303 <TEN>
A:Cross-references: EMBL:X59656; NID:q416519; PIDN:CAA42199.1; PID:q416520
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
F:14-102/Domain: SH2 homology <SH2>
F:130-178/Domain: SH3 homology <SH3>

Query Match 54.2%; Score 917.5; DB 2; Length 303;
Best Local Similarity 56.6%; Pred. No. 2.4e-61;
Matches 185; Conservative 33; Mismatches 56; Indels 53; Gaps 6;

QY 5 AGNFDSEERSWYGLSRQEAVALLOGRGVFLVRDSTSPGDYVLSVSENSRVSHYI 64
DB 3 SARFDSRSRAWYMGVPSRQEAQTRLOQRHGMFLVRDSTSPGDYVLSVSENSRVSHYI 62

QY 65 INSSGPRPPVPPSPAPQPPGVPSRLRGDQEFDSLPALEFYKIHLYDITTTLIEPVAR- 123
DB 63 INSLPNR-----RFGKIQDQEFDLPALEFYKIHLYDITTTLIEPAPRY 105

QY 124 -----SRQSGVILRQEAAYVRALEDFNGNDEEDLPFKKGDILIRDKPQEWNAED 177
DB 122 -----SRQSGVILRQEAAYVRALEDFNGNDEEDLPFKKGDILIRDKPQEWNAED 177

Db 106 PSPPMGVSAPNLPETAEDNLEYVRLTYDFPGNDAEDLPFKKGEILYIIEKPEQWMSARN 165
QY 178 SEGKRGIMPVYVEKYRPAASVSALIGGQEGSH-----PQPLGGPPG-PYAPQPSVN-- 230
Db 166 KDGRVGMIPVYVEK-----LYRSSPHKGHNNSNSYGIPEPAHAYAQPTTTP 215
QY 231 -----TDLPLNLQNGPIYARVQKRVNAYDKTALALEVGLVKVTKINVSQGW 278
Db 216 LPAVSGSPGAALPLPSTQNGPVFAKAIQKRVPCAYDKTALALEVGLVIVKVRNINQGW 275
QY 279 EGECKGRGHFPFTHVRLLDQONPDED 305
Db 276 EGEVNGRKGFLFPFTHVVKIFDPQNDEN 302

RESULT 7
S58352
SH2/SH3 adaptor protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 16-Jul-1999
C:Accession: S58352
R:de Jong, R.; Haataja, L.; Voncken, J.W.; Heisterkamp, N.; Groffen, J.
submitted to the EMBL Data Library, August 1995
A:Description: Tyrosine phosphorylation of murine Crkl.
A:Reference number: S58352
A:Accession: S58352
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-303 <DEJ>
A:Cross-references: EMBL:X90648; NID:g945008; PIDN:CAA62220.1; PID:g945009
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
F:14-102/Domain: SH2 homology <SH2>
F:130-178/Domain: SH3 homology <SH3>

Query Match 53.8%; Score 911.5; DB 2; Length 303;
Best Local Similarity 56.0%; Pred. No. 6.6e-61;
Matches 183; Conservative 34; Mismatches 57; Indels 53; Gaps 6;

QY 5 AGNFDSEERSWYGLSRQEAVALLOGRGVFLVRDSTSPGDYVLSVSENSRVSHYI 64
DB 3 SARFDSRSRAWYMGVPSRQEAQTRLOQRHGMFLVRDSTSPGDYVLSVSENSRVSHYI 62

QY 65 INSSGPRPPVPPSPAPQPPGVPSRLRGDQEFDSLPALEFYKIHLYDITTTLIEPVAR- 123
DB 63 INSLPNR-----RFGKIQDQEFDLPALEFYKIHLYDITTTLIEPAPRY 105

QY 124 -----SRQSGVILRQEAAYVRALEDFNGNDEEDLPFKKGDILIRDKPQEWNAED 177
DB 106 PSPPMGVSAPNLPETAEDNLEYVRLTYDFPGNDAEDLPFKKGEILYIIEKPEQWMSART 165

QY 178 SEGKRGIMPVYVEKYRPAASVSALIGGQEGSH-----PQPLGGPPG-PYAPQPSVNT 232
Db 166 KDGRVGMIPVYVEK-----LYRSSPHKGHNNSNSYGIPEPAHAYAQPTTTP 215

QY 233 LPNL-----QNGPIYARVQKRVNAYDKTALALEVGLVKVTKINVSQGW 278
Db 216 LPTVASTPAAINPLPSTQNGPVFAKAIQKRVPCAYDKTALALEVGLVIVKVRNINQGW 275

QY 279 EGECKGRGHFPFTHVRLLDQONPDED 305
Db 276 EGEVNGRKGFLFPFTHVVKIFDPQNDEN 302

RESULT 8
A44988
transforming protein (gag-crk) - avian sarcoma virus (fragments)
C:Species: avian sarcoma virus
C:Date: 28-Apr-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
C:Accession: A44988
R:Tsueh, H.; Chang, C.H.W.; Yoshida, M.; Vogt, P.K.
Oncogene 4, 1281-1284, 1989
A:Title: A newly isolated avian sarcoma virus, ASV-1, carries the crk oncogene.

Db 111 LRDC-----AGKFLWVVKFNSLNELVDYHR-----STS-----VSRNQ 144

QY 126 QGSGVILRQ-----EEAEYVRALFDNGNDEEDLPKKGDIILIRKPKPEQWNAEDSEG 180

Db 145 Q---IFLRDIEQVPQPTYYQALDFDQEDGELGFRRGDFIHVMDSNDFNWKGA-CHG 200

QY 181 KRGMPVPYV 190

Db 201 QTGMFPRNYV 210

RESULT 14

JT0664

growth factor receptor-binding protein GRB2 homolog - chicken

C:Species: Gallus gallus (chicken)

C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jan-2000

C:Accession: JT0664

R:Wasenius, V.M.; Merilaelinen, J.; Lehto, V.P.

Gene 134, 299-300, 1993

A:Title: Sequence of a chicken cDNA encoding a GRB2 protein.

A:Reference number: JT0664; MUID:94085795

A:Accession: JT0664

A:Molecule type: mRNA

A:Residues: 1-217 <WAS>

A:Cross-references: GB:I19258; NID:G304385; PIDN:AAAI6318.1; PID:G304386

C:Comment: GRB2 protein plays a role in mediating the critical linkage between growth factor receptor and Ras.

C:Superfamily: crk transforming protein; SH2 homology; SH3 homology

C:Keywords: growth factor receptor

F:5-53/Domain: SH3 homology <SH31>

F:60-150/Domain: SH2 homology <SH2>

F:163-210/Domain: SH3 homology <SH32>

Query Match 12.9%; Score 218; DB 2; Length 217;

Best Local Similarity 27.9%; Pred. No. 2.8e-09;

Matches 53; Conservative 44; Mismatches 57; Indels 36; Gaps 7;

QY 7 NFDSEERSWYWGRLSRQEAVALLOGRH-GVFLVRDSTSPGDYVLSVSENSRVSHYII 65

Db 51 NYIEMKPHWFFGKIPRAKAEMLGKORHDGAPLIRESSEAPGDFSLSVKFGNDVQOFKV 110

QY 66 NSSGPRPPVPPSPAQPPGVSPRLRIGDQFDSLPALLEFYKIHLYDTTLIEPVARS 125

Db 111 LRDC-----AGKYLWVVKFNSLNELVDYHR-----STS-----VSRNQ 144

QY 126 QGSGVILRQ-----EEAEYVRALFDNGNDEEDLPKKGDIILIRKPKPEQWNAEDSEG 180

Db 145 Q---IFLRDIEQVPQPTYYQALDFDQEDGELGFRRGDFIOVLNDSNDFNWKGA-CHG 200

QY 181 KRGMPVPYV 190

Db 201 QTGMFPRNYV 210

RESULT 15

S25730

SH2-SH3 protein sem-5 - Caenorhabditis elegans

N:Alternate names: sex-muscle-abnormal protein 5 (sem-5)

C:Species: Caenorhabditis elegans

C:Date: 25-Feb-1994 #sequence_revision 01-Sep-1995 #text_change 18-Aug-2000

C:Accession: S25730; T15499

R:Clark, S.G.; Stern, M.J.; Horvitz, H.R.

Nature 356, 340-344, 1992

A:Title: C. elegans cell-signalling gene sem-5 encodes a protein with SH2 and SH3 domain

A:Reference number: S25730; MUID:92195405

A:Accession: S25730

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-228 <CLA>

A:Cross-references: GB:S88446; NID:G247604; PID:G247605

R:Minx, P.

submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans cosmid C14F5.

A:Reference number: Z18361

A:Accession: T15499

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-228 <MIN>

A:Cross-references: EMBL:U29082; NID:G861384; PID:G861389; PIDN:AAA68405.1

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: sem-5

A:Introns: 26/3; 60/2; 101/2; 137/2; 183/1

C:Superfamily: crk transforming protein; SH2 homology; SH3 homology

F:5-53/Domain: SH3 homology <SH31>

F:60-151/Domain: SH2 homology <SH2>

F:161-208/Domain: SH3 homology <SH32>

Query Match 11.9%; Score 202; DB 2; Length 228;

Best Local Similarity 25.1%; Pred. No. 4.7e-08;

Matches 54; Conservative 39; Mismatches 68; Indels 54; Gaps 6;

QY 7 NFDSEERSWYWGRLSRQEAVALLOGQ--RHGVFLVRDSTSPGDYVLSVSENSRVSHYI 64

Db 51 NYIRWTECNWYLGKITRNDAEVLLKPTVRDGHFLVRQCESSPGFEFSISVRFQDSVQHF 110

QY 65 INSSGPRPPVPPSPAQPPGVSPSRLRIGDQ-----EFDSPALLEFYKIHLYDIT 115

Db 111 V-----LTDQNGKYYLWVVKFNSLNELVAYHRTASVSR 144

QY 116 TLIEPVARSROGSGVILRQ---EAQYVRALFDNGNDEEDLPKKGDIILIRKPKPEQW 172

Db 145 -----HTILLSDMNVEVKFQVALFDENFQESGELAFKRGDVTILNKDDPNW 191

QY 173 WNAEDSEGRGMIPVPYVVEKYRPPASASVSALIGN 207

Db 192 WEGQ-LNNRRRGIFPSNYVCPYNSKNKSNVAPGFN 225

Search completed: September 27, 2001, 16:42:23

Job time: 191 sec
